Geo-metagenomics: deciphering the spatial biodiversity of ssDNA viruses associated with Western Cape and Camargue agroecosystems .

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Over the past three years we have developed a geometagenomics approach which, based on the sampling design and the depth of sampling, enables the quantitative ecosystem-scale evaluation of spatial variations in, viral demographics, host distributions, and gene-flow. The approach is particularly well suited to analysing viral dynamics in ecosystem perturbations. The geometagenomics approach can precisely link individual sequence reads from bulked mixed sequencing reactions to information on abiotic and biotic conditions of the samples from which the sequences were obtained, the plant hosts from which samples were collected and the spatial arrangement of the samples. Our experimental design sampling locations are systematically placed within a predefined grid; the location of which is placed according to available geographic information systems data. This *a priori* choice of the sampling points allows the identification of reference ecosystems that should be appropriate for determining, for example, the impacts of agriculture on viral demographics and evolution within natural endangered ecosystems or the transmission rates of viruses between wild and cultivated plants.

Our study was conducted in the Western Cape (South Africa) and Camargue (France) regions, which include wild areas, including renosterveld shrubland and strandveld shrubland besides wide fertile plains under introduced crops such as barley, wheat and wine in South Africa and sansouires, marshes and meadows surrounded by areas under intensive agriculture such as rice and wheat in Camargue. Besides determining the spatial and host distributions of various groups of both known and previously unknown ssDNA viruses, we compare the ssDNA species richness of the various wild and cultivated sampling locations. Amongst a large number of apparently novel single stranded DNA viruses, was one in South Africa belonging to a new Geminivirus genus that we have tentatively named, Capulavirus.

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